

SEQUENCE LISTING

<110> Vanderbilt University  
Balser, Jeffrey R.  
5 George, Alfred L.  
Roden, Dan M.

<120> HUMAN KCR1 REGULATION OF HERG POTASSIUM CHANNEL BLOCK

10 <130> 1242-49

<150> 60/244,340  
<151> 2000-10-30

15 <160> 7

<170> PatentIn version 3.1

20 <210> 1  
<211> 1857  
<212> DNA  
<213> Homo sapiens

25 <220>  
<221> CDS  
<222> (1)..(1422)  
<223> n is any nucleotide

30 <220>  
<221> misc\_feature  
<222> (1)..(1857)  
<223> n is any nucleotide

35 <400> 1

atg gcg cag cta gag ggt tac tgt ttc tcg gcc gcc ttg agc tgt acc 48  
Met Ala Gln Leu Glu Gly Tyr Cys Phe Ser Ala Ala Leu Ser Cys Thr  
1 5 10 15

40 ttt tta gtg tcc tgc ctc ctc ttc tcc gcc ttc agc cgg gcg ctg cga 96  
Phe Leu Val Ser Cys Leu Leu Phe Ser Ala Phe Ser Arg Ala Leu Arg  
20 25 30

45 gag ccc tac atg gac gag atc ttc cac ctg cct cag gcg cag cgc tac 144  
Glu Pro Tyr Met Asp Glu Ile Phe His Leu Pro Gln Ala Gln Arg Tyr  
35 40 45

50 tgt gag ggc cat ttc tcc ctt tcc cag tgg gat ccc atg att act aca 192  
Cys Glu Gly His Phe Ser Leu Ser Gln Trp Asp Pro Met Ile Thr Thr  
50 55 60

55 tta cct ggc ttg tac ctg gtg tca gtt gga gtg gtc aaa cct gcc att 240  
Leu Pro Gly Leu Tyr Leu Val Ser Val Gly Val Val Lys Pro Ala Ile  
65 70 75 80

100000151.1030001

	tgg atc ttt gga tgg tct gaa cat gtt gtc tgc tcc att ggg atg ctc	288
	Trp Ile Phe Gly Trp Ser Glu His Val Val Cys Ser Ile Gly Met Leu	
	85 90 95	
5	aga ttt gtt aat ctt ctc ttc agt gtt ggc aac ttc tat tta cta tat	336
	Arg Phe Val Asn Leu Leu Phe Ser Val Gly Asn Phe Tyr Leu Leu Tyr	
	100 105 110	
10	ttg ctt ttc cac aag gta caa ccc aga aac aag gct gcc tca agt atc	384
	Leu Leu Phe His Lys Val Gln Pro Arg Asn Lys Ala Ala Ser Ser Ile	
	115 120 125	
15	cag aga gtc ttg tca aca tta aca cta gca gta ttt cca aca ctt tat	432
	Gln Arg Val Leu Ser Thr Leu Thr Leu Ala Val Phe Pro Thr Leu Tyr	
	130 135 140	
20	ttt ttt aac ttc ctt tat tat aca gaa gca gga tct atg ttt ttt act	480
	Phe Phe Asn Phe Leu Tyr Tyr Thr Glu Ala Gly Ser Met Phe Phe Thr	
	145 150 155 160	
25	ctt ttt gca tat ttg atg tgt ctt tat gga aat cat aaa act tca gcc	528
	Leu Phe Ala Tyr Leu Met Cys Leu Tyr Gly Asn His Lys Thr Ser Ala	
	165 170 175	
30	ttc ctt gga ttt tgt ggc ttc atg ttt cgg caa aca aat atc atc tgg	576
	Phe Leu Gly Phe Cys Gly Phe Met Phe Arg Gln Thr Asn Ile Ile Trp	
	180 185 190	
35	gct gtc ttc tgt gca ggg aat gtc att gca caa aag tta act gag gct	624
	Ala Val Phe Cys Ala Gly Asn Val Ile Ala Gln Lys Leu Thr Glu Ala	
	195 200 205	
40	tgg aaa act gag cta caa aag aag gaa gac aga ctt cca cct att aaa	672
	Trp Lys Thr Glu Leu Gln Lys Lys Glu Asp Arg Leu Pro Pro Ile Lys	
	210 215 220	
45	gga cca ttt gca gaa ttc aga aaa att ctt cag ttt ctt ttg gct tat	720
	Gly Pro Phe Ala Glu Phe Arg Lys Ile Leu Gln Phe Leu Leu Ala Tyr	
	225 230 235 240	
50	tcc atg tcc ttt aaa aac ttg agt atg ctt ttc tgt ttg act tgg ccc	768
	Ser Met Ser Phe Lys Asn Leu Ser Met Leu Phe Cys Leu Thr Trp Pro	
	245 250 255	
55	tac atc ctt ctg gga ttt ctg ttt tgt gct ttt gta gta gtt aat ggt	816
	Tyr Ile Leu Leu Gly Phe Leu Phe Cys Ala Phe Val Val Val Asn Gly	
	260 265 270	
60	gga att gtt att ggc gat cgg agt agt cat gaa gcc tgt ctt cat ttt	864
	Gly Ile Val Ile Gly Asp Arg Ser Ser His Glu Ala Cys Leu His Phe	
	275 280 285	
65	cct caa cta ttc tac ttt ttt tca ttt act ctc ttt ttt tct ttt cct	912
	Pro Gln Leu Phe Tyr Phe Phe Ser Phe Thr Leu Phe Phe Ser Phe Pro	
	290 295 300	

10000151-103001

	cat ctc ctg tct cct agc aaa att aag act ttt ctt tcc tta gtt tgg	960
	His Leu Leu Ser Pro Ser Lys Ile Lys Thr Phe Leu Ser Leu Val Trp	
	305 310 315 320	
5	aaa cat gga att ctg ttt ttg gtg gtt acc tta gtc tct gtg ttt tta	1008
	Lys His Gly Ile Leu Phe Leu Val Val Thr Leu Val Ser Val Phe Leu	
	325 330 335	
10	gtt tgg aaa ttc act tat gct cat aaa tac ttg cta gca gac aat aga	1056
	Val Trp Lys Phe Thr Tyr Ala His Lys Tyr Leu Leu Ala Asp Asn Arg	
	340 345 350	
15	cat tat act ttc tat gtg tgg aaa aga gtt ttt caa aga tat gca att	1104
	His Tyr Thr Phe Tyr Val Trp Lys Arg Val Phe Gln Arg Tyr Ala Ile	
	355 360 365	
20	ctg aaa tat ttg tta gtt cca gcc tat ata ttt gct ggt tgg agt ata	1152
	Leu Lys Tyr Leu Leu Val Pro Ala Tyr Ile Phe Ala Gly Trp Ser Ile	
	370 375 380	
25	gct gac tca ttg aaa tca aag cca att ttt tgg aat tta atg ttt ttc	1200
	Ala Asp Ser Leu Lys Ser Lys Pro Ile Phe Trp Asn Leu Met Phe Phe	
	385 390 395 400	
30	ata tgc ttg ttc att gtt ata gtt cct cag aaa ctg ctg gaa ttt cgt	1248
	Ile Cys Leu Phe Ile Val Ile Val Pro Gln Lys Leu Leu Glu Phe Arg	
	405 410 415	
35	tac ttc att tta cct tat gtc att tat agg ctt aac ata act ctg cct	1296
	Tyr Phe Ile Leu Pro Tyr Val Ile Tyr Arg Leu Asn Ile Thr Leu Pro	
	420 425 430	
40	ccc aca tcc aga ctt gtt tgt gaa ctg agt tgc tat gca att gtt aat	1344
	Pro Thr Ser Arg Leu Val Cys Glu Leu Ser Cys Tyr Ala Ile Val Asn	
	435 440 445	
45	ttc ata act ttt tac atc ttt ctg aac aag act ttt cag tgg cca aat	1392
	Phe Ile Thr Phe Tyr Ile Phe Leu Asn Lys Thr Phe Gln Trp Pro Asn	
	450 455 460	
50	agt cag gac att caa agg ttt atg tgg taa tatcagtgat attttgaact	1442
	Ser Gln Asp Ile Gln Arg Phe Met Trp	
	465 470	
55	gtaaaaatgg acttaataat agaccatttc taaaaagaac aactgaatag gnggaaaaca	1502
	tggaatttct tttaggtgca gtggtggtct tcaaattaca ttagtttttt taatatatat	1562
	tttaaacata tgtaagaaat taagtggcaa agaactggga aagcttaaga cctgcttcaa	1622
	angcctgaat aatgggaaaa taaanwngtt tncagatatc tcatatcgct cnnknatgn	1682
	tggcccytmn caangcttgg gaatgkttnn wntgnataag ttnattaaan ctgggnntgc	1742
	tnnmwatnac ttnnnkncca nccwnnnwac natgnnntan nnantattta caaaggtcag	1802
	gtgatattct tgactgaaaa gtgctctnaa cataaaagta aatatnggcc ncaaa	1857

10000151 "103001

```

<210> 2
<211> 473
5 <212> PRT
  <213> Homo sapiens

<220>
<221> misc_feature
10 <222> (1)..(1857)
  <223> n is any nucleotide
  <400> 2

Met Ala Gln Leu Glu Gly Tyr Cys Phe Ser Ala Ala Leu Ser Cys Thr
15 1 5 10 15

Phe Leu Val Ser Cys Leu Leu Phe Ser Ala Phe Ser Arg Ala Leu Arg
20 20 25 30

Glu Pro Tyr Met Asp Glu Ile Phe His Leu Pro Gln Ala Gln Arg Tyr
25 35 40 45

Cys Glu Gly His Phe Ser Leu Ser Gln Trp Asp Pro Met Ile Thr Thr
50 55 60

Leu Pro Gly Leu Tyr Leu Val Ser Val Gly Val Val Lys Pro Ala Ile
65 70 75 80

Trp Ile Phe Gly Trp Ser Glu His Val Val Cys Ser Ile Gly Met Leu
30 85 90 95

Arg Phe Val Asn Leu Leu Phe Ser Val Gly Asn Phe Tyr Leu Leu Tyr
100 105 110

Leu Leu Phe His Lys Val Gln Pro Arg Asn Lys Ala Ala Ser Ser Ile
35 115 120 125

Gln Arg Val Leu Ser Thr Leu Thr Leu Ala Val Phe Pro Thr Leu Tyr
40 130 135 140

Phe Phe Asn Phe Leu Tyr Tyr Thr Glu Ala Gly Ser Met Phe Phe Thr
145 150 155 160

Leu Phe Ala Tyr Leu Met Cys Leu Tyr Gly Asn His Lys Thr Ser Ala
45 165 170 175

Phe Leu Gly Phe Cys Gly Phe Met Phe Arg Gln Thr Asn Ile Ile Trp
180 185 190

Ala Val Phe Cys Ala Gly Asn Val Ile Ala Gln Lys Leu Thr Glu Ala
50 195 200 205

Trp Lys Thr Glu Leu Gln Lys Lys Glu Asp Arg Leu Pro Pro Ile Lys
210 215 220

Gly Pro Phe Ala Glu Phe Arg Lys Ile Leu Gln Phe Leu Leu Ala Tyr
55 225 230 235 240

```

10000151-103001

Ser Met Ser Phe Lys Asn Leu Ser Met Leu Phe Cys Leu Thr Trp Pro  
 245 250 255  
 5 Tyr Ile Leu Leu Gly Phe Leu Phe Cys Ala Phe Val Val Val Asn Gly  
 260 265 270  
 Gly Ile Val Ile Gly Asp Arg Ser Ser His Glu Ala Cys Leu His Phe  
 275 280 285  
 10 Pro Gln Leu Phe Tyr Phe Phe Ser Phe Thr Leu Phe Phe Ser Phe Pro  
 290 295 300  
 His Leu Leu Ser Pro Ser Lys Ile Lys Thr Phe Leu Ser Leu Val Trp  
 15 305 310 315 320  
 Lys His Gly Ile Leu Phe Leu Val Val Thr Leu Val Ser Val Phe Leu  
 325 330 335  
 20 Val Trp Lys Phe Thr Tyr Ala His Lys Tyr Leu Leu Ala Asp Asn Arg  
 340 345 350  
 His Tyr Thr Phe Tyr Val Trp Lys Arg Val Phe Gln Arg Tyr Ala Ile  
 355 360 365  
 25 Leu Lys Tyr Leu Leu Val Pro Ala Tyr Ile Phe Ala Gly Trp Ser Ile  
 370 375 380  
 Ala Asp Ser Leu Lys Ser Lys Pro Ile Phe Trp Asn Leu Met Phe Phe  
 30 385 390 395 400  
 Ile Cys Leu Phe Ile Val Ile Val Pro Gln Lys Leu Leu Glu Phe Arg  
 405 410 415  
 35 Tyr Phe Ile Leu Pro Tyr Val Ile Tyr Arg Leu Asn Ile Thr Leu Pro  
 420 425 430  
 Pro Thr Ser Arg Leu Val Cys Glu Leu Ser Cys Tyr Ala Ile Val Asn  
 435 440 445  
 40 Phe Ile Thr Phe Tyr Ile Phe Leu Asn Lys Thr Phe Gln Trp Pro Asn  
 450 455 460  
 Ser Gln Asp Ile Gln Arg Phe Met Trp  
 45 465 470  
 <210> 3  
 <211> 1159  
 50 <212> PRT  
 <213> Homo sapiens  
 <400> 3  
 55 Met Pro Val Arg Arg Gly His Val Ala Pro Gln Asn Thr Phe Leu Asp  
 1 5 10 15

10000151-103001

	Thr	Ile	Ile	Arg	Lys	Phe	Glu	Gly	Gln	Ser	Arg	Lys	Phe	Ile	Ile	Ala	
				20					25					30			
5	Asn	Ala	Arg	Val	Glu	Asn	Cys	Ala	Val	Ile	Tyr	Cys	Asn	Asp	Gly	Phe	
			35					40					45				
	Cys	Glu	Leu	Cys	Gly	Tyr	Ser	Arg	Ala	Glu	Val	Met	Gln	Arg	Pro	Cys	
		50					55					60					
10	Thr	Cys	Asp	Phe	Leu	His	Gly	Pro	Arg	Thr	Gln	Arg	Arg	Ala	Ala	Ala	
	65					70					75					80	
	Gln	Ile	Ala	Gln	Ala	Leu	Leu	Gly	Ala	Glu	Glu	Arg	Lys	Val	Glu	Ile	
					85					90					95		
15	Ala	Phe	Tyr	Arg	Lys	Asp	Gly	Ser	Cys	Phe	Leu	Cys	Leu	Val	Asp	Val	
				100					105					110			
	Val	Pro	Val	Lys	Asn	Glu	Asp	Gly	Ala	Val	Ile	Met	Phe	Ile	Leu	Asn	
20				115				120					125				
	Phe	Glu	Val	Val	Met	Glu	Lys	Asp	Met	Val	Gly	Ser	Pro	Ala	His	Asp	
		130					135					140					
25	Thr	Asn	His	Arg	Gly	Pro	Pro	Thr	Ser	Trp	Leu	Ala	Pro	Gly	Arg	Ala	
	145					150					155					160	
	Lys	Thr	Phe	Arg	Leu	Lys	Leu	Pro	Ala	Leu	Leu	Ala	Leu	Thr	Ala	Arg	
					165					170					175		
30	Glu	Ser	Ser	Val	Arg	Ser	Gly	Gly	Ala	Gly	Gly	Ala	Gly	Ala	Pro	Gly	
				180				185						190			
	Ala	Val	Val	Val	Asp	Val	Asp	Leu	Thr	Pro	Ala	Ala	Pro	Ser	Ser	Glu	
35			195					200					205				
	Ser	Leu	Ala	Leu	Asp	Glu	Val	Thr	Ala	Met	Asp	Asn	His	Val	Ala	Gly	
		210					215				220						
40	Leu	Gly	Pro	Ala	Glu	Glu	Arg	Arg	Ala	Leu	Val	Gly	Pro	Gly	Ser	Pro	
	225					230					235					240	
	Pro	Arg	Ser	Ala	Pro	Gly	Gln	Leu	Pro	Ser	Pro	Arg	Ala	His	Ser	Leu	
				245					250					255			
45	Asn	Pro	Asp	Ala	Ser	Gly	Ser	Ser	Cys	Ser	Leu	Ala	Arg	Thr	Arg	Ser	
				260					265					270			
	Arg	Glu	Ser	Cys	Ala	Ser	Val	Arg	Arg	Ala	Ser	Ser	Ala	Asp	Asp	Ile	
50			275					280					285				
	Glu	Ala	Met	Arg	Ala	Gly	Val	Leu	Pro	Pro	Pro	Pro	Arg	His	Ala	Ser	
		290					295					300					
55	Thr	Gly	Ala	Met	His	Pro	Leu	Arg	Ser	Gly	Leu	Leu	Asn	Ser	Thr	Ser	
	305					310					315					320	

10000151.103004

	Asp Ser Asp Leu Val Arg Tyr Arg Thr Ile Ser Lys Ile Pro Gln Ile	325	330	335
5	Thr Leu Asn Phe Val Asp Leu Lys Gly Asp Pro Phe Leu Ala Ser Pro	340	345	350
	Thr Ser Asp Arg Glu Ile Ile Ala Pro Lys Ile Lys Glu Arg Thr His	355	360	365
10	Asn Val Thr Glu Lys Val Thr Gln Val Leu Ser Leu Gly Ala Asp Val	370	375	380
	Leu Pro Glu Tyr Lys Leu Gln Ala Pro Arg Ile His Arg Trp Thr Ile	385	390	395
15	Leu His Tyr Ser Pro Phe Lys Ala Val Trp Asp Trp Leu Ile Leu Leu	405	410	415
20	Leu Val Ile Tyr Thr Ala Val Phe Thr Pro Tyr Ser Ala Ala Phe Leu	420	425	430
	Leu Lys Glu Thr Glu Glu Gly Pro Pro Ala Thr Glu Cys Gly Tyr Ala	435	440	445
25	Cys Gln Pro Leu Ala Val Val Asp Leu Ile Val Asp Ile Met Phe Ile	450	455	460
	Val Asp Ile Leu Ile Asn Phe Arg Thr Thr Tyr Val Asn Ala Asn Glu	465	470	475
30	Glu Val Val Ser His Pro Gly Arg Ile Ala Val His Tyr Phe Lys Gly	485	490	495
	Trp Phe Leu Ile Asp Met Val Ala Ala Ile Pro Phe Asp Leu Leu Ile	500	505	510
35	Phe Gly Ser Gly Ser Glu Glu Leu Ile Gly Leu Leu Lys Thr Ala Arg	515	520	525
40	Leu Leu Arg Leu Val Arg Val Ala Arg Lys Leu Asp Arg Tyr Ser Glu	530	535	540
	Tyr Gly Ala Ala Val Leu Phe Leu Leu Met Cys Thr Phe Ala Leu Ile	545	550	555
45	Ala His Trp Leu Ala Cys Ile Trp Tyr Ala Ile Gly Asn Met Glu Gln	565	570	575
	Pro His Met Asp Ser Arg Ile Gly Trp Leu His Asn Leu Gly Asp Gln	580	585	590
50	Ile Gly Lys Pro Tyr Asn Ser Ser Gly Leu Gly Gly Pro Ser Ile Lys	595	600	605
55	Asp Lys Tyr Val Thr Ala Leu Tyr Phe Thr Phe Ser Ser Leu Thr Ser	610	615	620

10000151.103001

	Val	Gly	Phe	Gly	Asn	Val	Ser	Pro	Asn	Thr	Asn	Ser	Glu	Lys	Ile	Phe	625	630	635	640
5	Ser	Ile	Cys	Val	Met	Leu	Ile	Gly	Ser	Leu	Met	Tyr	Ala	Ser	Ile	Phe	645	650	655	
	Gly	Asn	Val	Ser	Ala	Ile	Ile	Gln	Arg	Leu	Tyr	Ser	Gly	Thr	Ala	Arg	660	665	670	
10	Tyr	His	Thr	Gln	Met	Leu	Arg	Val	Arg	Glu	Phe	Ile	Arg	Phe	His	Gln	675	680	685	
	Ile	Pro	Asn	Pro	Leu	Arg	Gln	Arg	Leu	Glu	Glu	Tyr	Phe	Gln	His	Ala	690	695	700	
15	Trp	Ser	Tyr	Thr	Asn	Gly	Ile	Asp	Met	Asn	Ala	Val	Leu	Lys	Gly	Phe	705	710	715	720
20	Pro	Glu	Cys	Leu	Gln	Ala	Asp	Ile	Cys	Leu	His	Leu	Asn	Arg	Ser	Leu	725	730	735	
	Leu	Gln	His	Cys	Lys	Pro	Phe	Arg	Gly	Ala	Thr	Lys	Gly	Cys	Leu	Arg	740	745	750	
25	Ala	Leu	Ala	Met	Lys	Phe	Lys	Thr	Thr	His	Ala	Pro	Pro	Gly	Asp	Thr	755	760	765	
	Leu	Val	His	Ala	Gly	Asp	Leu	Leu	Thr	Ala	Leu	Tyr	Phe	Ile	Ser	Arg	770	775	780	
30	Gly	Ser	Ile	Glu	Ile	Leu	Arg	Gly	Asp	Val	Val	Val	Ala	Ile	Leu	Gly	785	790	795	800
	Lys	Asn	Asp	Ile	Phe	Gly	Glu	Pro	Leu	Asn	Leu	Tyr	Ala	Arg	Pro	Gly	805	810	815	
35	Lys	Ser	Asn	Gly	Asp	Val	Arg	Ala	Leu	Thr	Tyr	Cys	Asp	Leu	His	Lys	820	825	830	
40	Ile	His	Arg	Asp	Asp	Leu	Leu	Glu	Val	Leu	Asp	Met	Tyr	Pro	Glu	Phe	835	840	845	
	Ser	Asp	His	Phe	Trp	Ser	Ser	Leu	Glu	Ile	Thr	Phe	Asn	Leu	Arg	Asp	850	855	860	
45	Thr	Asn	Met	Ile	Pro	Gly	Ser	Pro	Gly	Ser	Thr	Glu	Leu	Glu	Gly	Gly	865	870	875	880
	Phe	Ser	Arg	Gln	Arg	Lys	Arg	Lys	Leu	Ser	Phe	Arg	Arg	Arg	Thr	Asp	885	890	895	
50	Lys	Asp	Thr	Glu	Gln	Pro	Gly	Glu	Val	Ser	Ala	Leu	Gly	Pro	Gly	Arg	900	905	910	
55	Ala	Gly	Ala	Gly	Pro	Ser	Ser	Arg	Gly	Arg	Pro	Gly	Gly	Pro	Trp	Gly	915	920	925	

10000151 "103001



Glu Ser Pro Ser Ser Gly Pro Ser Ser Pro Glu Ser Ser Glu Asp Glu  
 930 935 940  
 Gly Pro Gly Arg Ser Ser Pro Leu Arg Leu Val Pro Phe Ser Ser  
 5 945 950 955 960  
 Pro Arg Pro Pro Gly Glu Pro Pro Gly Gly Glu Pro Leu Met Glu Asp  
 965 970 975  
 10 Cys Glu Lys Ser Ser Asp Thr Cys Asn Pro Leu Ser Gly Ala Phe Ser  
 980 985 990  
 Gly Val Ser Asn Ile Phe Ser Phe Trp Gly Asp Ser Arg Gly Arg Gln  
 995 1000 1005  
 15 Tyr Gln Glu Leu Pro Arg Cys Pro Ala Pro Thr Pro Ser Leu Leu  
 1010 1015 1020  
 Asn Ile Pro Leu Ser Ser Pro Gly Arg Arg Pro Arg Gly Asp Val  
 20 1025 1030 1035  
 Glu Ser Arg Leu Asp Ala Leu Gln Arg Gln Leu Asn Arg Leu Glu  
 1040 1045 1050  
 25 Thr Arg Leu Ser Ala Asp Met Ala Thr Val Leu Gln Leu Leu Gln  
 1055 1060 1065  
 Arg Gln Met Thr Leu Val Pro Pro Ala Tyr Ser Ala Val Thr Thr  
 1070 1075 1080  
 30 Pro Gly Pro Gly Pro Thr Ser Thr Ser Pro Leu Leu Pro Val Ser  
 1085 1090 1095  
 Pro Leu Pro Thr Leu Thr Leu Asp Ser Leu Ser Gln Val Ser Gln  
 35 1100 1105 1110  
 Phe Met Ala Cys Glu Glu Leu Pro Pro Gly Ala Pro Glu Leu Pro  
 1115 1120 1125  
 40 Gln Glu Gly Pro Thr Arg Arg Leu Ser Leu Pro Gly Gln Leu Gly  
 1130 1135 1140  
 Ala Leu Thr Ser Gln Pro Leu His Arg His Gly Ser Asp Pro Gly  
 1145 1150 1155  
 45 Ser

50 <210> 4  
 <211> 732  
 <212> DNA  
 <213> Homo sapiens  
 55 <220>  
 <221> CDS  
 <222> (74) .. (445)  
 <223>

1000151.103001

<400> 4

5 caaatccaga aaagatccgt tttcctaacc ttgttcgcct attttattat ttaaattgca 60  
gcaggaggga agc atg tct act tta tcc aat ttc aca cag acg ctg gaa 109  
Met Ser Thr Leu Ser Asn Phe Thr Gln Thr Leu Glu  
1 5 10  
10 gac gtc ttc cga agg att ttt att act tat atg gac aat tgg cgc cag 157  
Asp Val Phe Arg Arg Ile Phe Ile Thr Tyr Met Asp Asn Trp Arg Gln  
15 20 25  
15 aac aca aca gct gag caa gag gcc ctc caa gcc aaa gtt gat gct gag 205  
Asn Thr Thr Ala Glu Gln Glu Ala Leu Gln Ala Lys Val Asp Ala Glu  
30 35 40  
20 aac ttc tac tat gtc atc ctg tac ctc atg gtg atg att gga atg ttc 253  
Asn Phe Tyr Tyr Val Ile Leu Tyr Leu Met Val Met Ile Gly Met Phe  
45 50 55 60  
25 tct ttc atc atc gtg gcc atc ctg gtg agc act gtg aaa tcc aag aga 301  
Ser Phe Ile Ile Val Ala Ile Leu Val Ser Thr Val Lys Ser Lys Arg  
65 70 75  
30 cgg gaa cac tcc aat gac ccc tac cac cag tac att gta gag gac tgg 349  
Arg Glu His Ser Asn Asp Pro Tyr His Gln Tyr Ile Val Glu Glu Ser Lys Trp  
80 85 90  
35 cag gaa aag tac aag agc caa atc ttg aat cta gaa gaa tcg aag gcc 397  
Gln Glu Lys Tyr Lys Ser Gln Ile Leu Asn Leu Glu Glu Ser Lys Ala  
95 100 105  
40 acc atc cat gag aac att ggt gcg gct ggg ttc aaa atg tcc ccc tga 445  
Thr Ile His Glu Asn Ile Gly Ala Ala Gly Phe Lys Met Ser Pro  
110 115 120  
45 taagggagaa aggcaccaag ctaacatctg acgtccagac atgaagagat gccagtgcca 505  
cgaggcaaat ccaaattgtc tttgcttaga agaaagttag ttccttgctc tctgttgaga 565  
attttcatgg agattatgtg gttggccaat aaagatagat gacatttcaa tctcagtgat 625  
ttatgcttgc ttgttggagc aatattttgt gctgaagacc tcttttactt tccgggcaag 685  
tgaatgtcat tttaatcaat atcaatgatg aaaataaagc caaattt 732  
50 <210> 5  
<211> 123  
<212> PRT  
<213> Homo sapiens  
55 <400> 5

10000151.103001

Met Ser Thr Leu Ser Asn Phe Thr Gln Thr Leu Glu Asp Val Phe Arg  
1 5 10 15

5 Arg Ile Phe Ile Thr Tyr Met Asp Asn Trp Arg Gln Asn Thr Thr Ala  
20 25 30

Glu Gln Glu Ala Leu Gln Ala Lys Val Asp Ala Glu Asn Phe Tyr Tyr  
35 40 45

10 Val Ile Leu Tyr Leu Met Val Met Ile Gly Met Phe Ser Phe Ile Ile  
50 55 60

15 Val Ala Ile Leu Val Ser Thr Val Lys Ser Lys Arg Arg Glu His Ser  
65 70 75 80

Asn Asp Pro Tyr His Gln Tyr Ile Val Glu Asp Trp Gln Glu Lys Tyr  
85 90 95

20 Lys Ser Gln Ile Leu Asn Leu Glu Glu Ser Lys Ala Thr Ile His Glu  
100 105 110

Asn Ile Gly Ala Ala Gly Phe Lys Met Ser Pro  
115 120

25 <210> 6  
<211> 21  
<212> DNA  
<213> Synthetic

30 <400> 6

tttcaaagat atgcaattct g 21

35 <210> 7  
<211> 20  
<212> DNA  
<213> Synthetic

40 <400> 7

aagtcattt ttacagttca 20

10000151.103001